

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: \(\)

Source:

Date Processed by STIC:

and Processed by STIC.

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (http://www.uspto.gov/ebc/efs/downloads/documents.htm, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
- Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
 U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

	DO1/100 Q1/
ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 04 48 184
LTTN: NEW RULES CASES:	PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY 1TO SOFTWARE
Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was reflieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers: use space characters, instead.
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
SVariable Length	Sequence(s) contain n's or X22's representing more than one residue. Per Sequence Rules, each n or X22 can only represent a slugle residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing
6Patentin 2.0 "bug"	A "bug" in Patentin version 2.0 has caused the <220>-<223> section to be missing from anino acid sequences(s) Normally, Patentin would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7Skipped Sequences (OLD RULES)	Sequence(s) missing If intentional, please insert the following lines for each skipped sequence (2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this leading) (xi) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped
	Please also adjust the "(n) NUMBER OF SEQUENCES" response to include the skipped sequences.
8 Skipped Sequences (NEW RULES)	Sequence(s)
9 Use of his or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1-823 of Sequence Rules, use of <220> <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10 Invalid <213> Response	Per 1-823 of Sequence Rules, the only valid <213> responses are. Unknown, Artificial Sequence, or scientific name (Genus/species). <220>.<223> section is required when <213> response is Unknown or is Artificial Sequence.
Usc of <270>	Sequence(s)
Patentle 2.0 "bug"	Please do not use "Copy to Disk" function of Patentln version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13 Misuse of n/X22	"n" can only represent a single nucleotide; "X22" can only represent a single amino acid

AMC - Biotechnology Systems Dranch - 09/09/2003



IFW16

RAW SEQUENCE LISTING

DATE: 12/22/2004

PATENT APPLICATION: US/09/487,841

TIME: 15:09:45

Input Set : A:\seqlist.txt

Output Set: N:\CRF4\12222004\I487841.raw

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4 <110> APPLICANT: Gravel, Roy A,
        Rozen, Rima
       Leclerc, Daniel
       Wilson, Aaron
7
       Rosenblatt, David
```

- 10 <120> TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
- CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
- DEFECTS, CARDIOVASCULAR DISEASE, CANCER, AND DOWN'S SYNDROME 12
- 15 <130> FILE REFERENCE: 50004/003004
- 17 <140> CURRENT APPLICATION NUMBER: 09/487,841
- 18 <141> CURRENT FILING DATE: 2000-01-19
- 20 <150> PRIOR APPLICATION NUMBER: 09/371,347
- 21 <151> PRIOR FILING DATE: 1999-08-10
- 23 <150> PRIOR APPLICATION NUMBER: 09/232,028
- 24 <151> PRIOR FILING DATE: 1999-01-15
- 26 <150> PRIOR APPLICATION NUMBER: 60/071,622
- 27 <151> PRIOR FILING DATE: 1998-01-16
- 29 <160> NUMBER OF SEQ ID NOS: 61
- 31 <170> SOFTWARE: FastSEQ for Windows Version 4.0

Dres Not Comply Corrected Diskette Needed

9.3,5-19,12,14,16

ERRORED SEQUENCES

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- 325 Ala Asp Leu His Cys Ile Ser Glu Ser Asp Lys Tyr Asp Leu Lys Thr
- 327 Glu Thr Ala Pro Leu Val Val Val Ser Thr Thr Gly Thr Gly Asp
- 329 Pro Pro Asp Thr Ala Arg Lys Phe Val Lys Glu Ile Gln Asn Gln Thr
- 330 65 70 331 Leu Pro Val Asp Phe Phe Ala His Leu Arg Tyr Gly Leu Leu Gly Leu
- 333 Gly Asp Ser Glu Tyr Thr Tyr Phe Cys Asn Gly Gly Lys Ile Ile Asp 100 105
- 335 Lys Arg Leu Gln Glu Leu Gly Ala Arg His Phe Tyr Asp Thr Gly His

Input Set : A:\seqlist.txt

226			115					120					125			
336		7 an		Cvc	175 T	Gly	T 011		T 011	17 ~]	17-1	Clu		Tro	т1Б	712
	нта	_	мър	Cys	vaı	GIY		GIU	пец	val	vai		FIU	тър	116	AIG
338	~1	130		D	7 T _	T	135	-	TT -	Dl	7	140	0	7	01	<i>α</i> 1
	_	Leu	Trp	Pro	Ата	Leu	Arg	ьуѕ	HIS	Pne	_	ser	ser	Arg	GIY	
	145			_		150	_	_			155	_		_	_	160
	GIu	GIu	Ile	Ser	_	Ala	Leu	Pro	Val		ser	Pro	Ala	ser		Arg
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3 4 8		210					215					220				
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351	Asn	Ile	Pro	Gly	Leu	Pro	Pro	Glu	Tyr	Leu	Gln	Val	His	Leu	Gln	Glu
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356			275					280					285			-
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358		290	•				295				+	300				-
359	Phe	Ser	Tvr	Gln	Pro	Gly	Asp	Ala	Phe	Ser	Val	Ile	Cys	Pro	Asn	Ser
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		Ser	Glu	Val	Gln	Ser	Leu	Leu	Gln	Ara		Gln	Leu	Glu	Asp	Lvs
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364				340				-1-	345	-1-				350	-1-	-1-
	Glv	Δla	Thr		Pro	Gln	His	Tle		Ala	Glv	Cvs	Ser		Gln	Phe
366	_	1114	355	200		0111		360			0-1	•1.0	365		V	
		Phe		Trn	Cvs	Leu	G] 11		Δra	Δla	Tle	Pro		Lvs	Δla	Phe
368		370	1111	111	Cyb	шец	375	110	****9	1114		380	Lys		1114	2110
			Δla	T.011	Val	Asp		Thr	Ser	Asn	Ser		Glu	Lvs	Δra	Ara
	385	**** 9	1124	шеш	• 41	390	- 1 -		001	T.DP	395	*****	014		**** 9	400
		Gln	Glu	T.eu	Cvc	Ser	Lvc	Gln	Gl v	Δla		Asn	Tyr	Ser	Ara	
372	Lou	0111	014	Leu	405	DC1	2,2	0111	0- <i>j</i>	410			-1-	501	415	2 220
	Val	Δra	Acn	Δla		Ala	Cvc	T.011	I.e.11		T. - 311	T.e.11	T.e.11	Δla		Pro
374	VUL	rrg	лър	420	Cys	пла	СуБ	пси	425	нор	пси	пси	ыса	430	1110	110
	Sar	Carc	Cln.		Dro	Leu	Cor	Leu		T.611	Glu	Hic	T.011		Lare	T. - 211
376	ser	Cys	435	PIO	PLO	пец	per	440	Бец	пеа	Gru	1112	445	PIQ	цур	пец
	~1 n	Droo		Dwo	TTr ***	Com	C++0		Com	Cox	Cox	T 011		II.	Dro	C1
	GTII		Arg	PLO	TAT	Ser	_	WIG	ser	SGT	PET		Fire	пты	FIO	GIA
378	T	450	TT# -	D1	77e 7	Dl	455	- 7 -	77- 7	al.	Dl	460	0	ml		mb
	_	ьeu	HIS	rne	vaı	Phe	Asn	тте	vaı	GIU		ьeu	ser	ınr	Ата	
	465	a 3		_	_	470	~ 7		a	m)	475	m	-		.	480
	Thr	Glu	val	Leu		Lys	GTA	val	cys		GTA	Trp	ьeu	Ala		ьeu
382			_		485		_	_		490		_			495	
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Input Set : A:\seqlist.txt

Output Set: N:\CRF4\12222004\I487841.raw

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435 Thr Glu Glu Lys Lys Ala Leu Leu Gln Lys Arg Ile Glu Asp Glu

Input Set : A:\seqlist.txt

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447	Pro	Phe	Glu	Val	Leu	Val	Val	Ser	Ala	Glu	Phe	Val	Thr	Asp	Pro	Phe
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4 53	Val	Pro	Asn	Pro	Ala	Leu	Glu	Val	Asn	Phe	Ile	Leu	Lys	Arg	Cys	Gly
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458			355					360					365			
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460		370					375			_		380				
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	385	_	_	_	_	390	~ 7	_	_	_	395	~7	~7		.	400
	Glu	Lys	Arg	Arg		Leu	GIu	Leu	Cys		Ala	GIn	GIY	мет		
464	m 1	m1		D1	405	7	(T)]	D	a 3	410	C	T	7. T	7. ~~~	415	
	Phe	Tnr	Asp		vai	Arg	Ini	PIO	425	ьeu	ser	ьец	ALA	430	Mec	пец
466	Phe	ח ד ת	Dho	420	7 an	T/al	Tara	Dro		Tz-1	7) cm	Ara	Lou		Glu	T.011
468	PHE	Ата	435	PIO	ASII	vaı	цув	440	FIO	Val	АЗР	nr 9	445	110	OLu	шеи
	Leu	Pro		T.e.11	Tle	Pro	Ara		Tyr	Ser	Met	Ser		Tvr	G] 11	Asn
470	шси	450	my	ЦСИ	110	110	455	110	- 1 -	DOL	1100	460	DOL	-1-	014	
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474	•	J	,		485		-	•		490		-	-		495	
475	Leu	Arq	Ile	Gly	Asp	Lys	Val	Gln	Val	Leu	Gly	Lys	Glu	Pro	Ala	Arg
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477	Phe	Arg	Leu	Pro	Pro	Leu	Gly	Met	Thr	Lys	Asn	Ser	Ala	Gly	Lys	Leu
478		-	515					520					525			
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483	Val	Asp	Val	Pro	Arg	Val	Leu	Phe	Phe		Cys	Arg	Asp	Ser		Val
484					565					570					575	

DATE: 12/22/2004

TIME: 15:09:45

Input Set : A:\seqlist.txt Output Set: N:\CRF4\12222004\I487841.raw 485 Asp Ala Ile Tyr Met Ser Glu Leu Glu Met Phe Val Ser Glu Gly Ile 580 585 487 Leu Thr Asp Leu Ile Ile Cys Glu Ser Glu Gln Lys Gly Glu Arg Val 595 600 489 Gln Asp Gly Leu Arg Lys Tyr Leu Asp Lys Val Leu Pro Phe Leu Thr. 615 491 Ala Ser Thr Glu Ser Lys Ile Phe Ile Cys Gly Asp Ala Lys Gly Met 630 635 493 Ser Lys Asp Val Trp Gln Cys Phe Ser Asp Ile Val Ala Ser Asp Gln-645 650 E--> 495 Gly Ile Pro Asp Leu Glu Ala Lys Lys Leu Met Asp Leu Lys Lys 660 497 <210> SEQ ID NO: 23 498 <211> LENGTH: 677 499 <212> TYPE: PRT 500 <213> ORGANISM: Homo sapiens 502 <400> SEQUENCE: 23 E--> 503 Met Gly Asp Ser His Val Asp Thr Ser Ser Thr Val Ser Glu Ala Val 504 1 505 Ala Glu Glu Val Ser Leu Phe Ser Met Thr Asp Met Ile Leu Phe Ser 20 25 507 Leu Ile Val Gly Leu Leu Thr Tyr Trp Phe Leu Phe Arg Lys Lys 509 Glu Glu Val Pro Glu Phe Thr Lys Ile Gln Thr Leu Thr Ser Ser Val 511 Arg Glu Ser Ser Phe Val Glu Lys Met Lys Lys Thr Gly Arg Asn Ile 513 Ile Val Phe Tyr Gly Ser Gln Thr Gly Thr Ala Glu Glu Phe Ala Asn 85 90 515 Arg Leu Ser Lys Asp Ala His Arg Tyr Gly Met Arg Gly Met Ser Ala 105 517 Asp Pro Glu Glu Tyr Asp Leu Ala Asp Leu Ser Ser Leu Pro Glu Ile 120 519 Asp Asn Ala Leu Val Val Phe Cys Met Ala Thr Tyr Gly Glu Gly Asp 135 521 Pro Thr Asp Asn Ala Gln Asp Phe Tyr Asp Trp Leu Gln Glu Thr Asp 150 155 522 145 523 Val Asp Leu Ser Gly Val Lys Phe Ala Val Phe Gly Leu Gly Asn Lys 165 170 525 Thr Tyr Glu His Phe Asn Ala Met Gly Lys Tyr Val Asp Lys Arg Leu 185 527 Glu Gln Leu Gly Ala Gln Arg Ile Phe Glu Leu Gly Leu Gly Asp Asp 200 529 Asp Gly Asn Leu Glu Glu Asp Phe Ile Thr Trp Arg Glu Gln Phe Trp 210 215 531 Pro Ala Val Cys Glu His Phe Gly Val Glu Ala Thr Gly Glu Glu Ser 230 235 533 Ser Ile Arq Gln Tyr Glu Leu Val Val His Thr Asp Ile Asp Ala Ala 245 250 535 Lys Val Tyr Met Gly Glu Met Gly Arg Leu Lys Ser Tyr Glu Asn Gln

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/487,841

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PATENT APPLICATION: US/09/487,841 TIME: 15:09:45

DATE: 12/22/2004

Input Set : A:\seqlist.txt

Output Set: N:\CRF4\12222004\I487841.raw

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537 Lys Pro Pro Phe Asp Ala Lys Asn Pro Phe Leu Ala Ala Val Thr Thr
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539 Asn Arg Lys Leu Asn Gln Gly Thr Glu Arg His Leu Met His Leu Glu
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541 Leu Asp Ile Ser Asp Ser Lys Ile Arg Tyr Glu Ser Gly Asp His Val
                       310
                                          315
543 Ala Val Tyr Pro Ala Asn Asp Ser Ala Leu Val Asn Gln Leu Gly Lys
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                                      330
545 Ile Leu Gly Ala Asp Leu Asp Val Val Met Ser Leu Asn Asn Leu Asp
               340
                                   345
547 Glu Glu Ser Asn Lys Lys His Pro Phe Pro Cys Pro Thr Ser Tyr Arg
548
           355
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549 Thr Ala Leu Thr Tyr Tyr Leu Asp Ile Thr Asn Pro Pro Arg Thr Asn
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551 Val Leu Tyr Glu Leu Ala Gln Tyr Ala Ser Glu Pro Ser Glu Gln Glu
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553 Leu Leu Arq Lys Met Ala Ser Ser Ser Gly Glu Gly Lys Glu Leu Tyr
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555 Leu Ser Trp Val Val Glu Ala Arg Arg His Ile Leu Ala Ile Leu Gln
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557 Asp Cys Pro Ser Leu Arg Pro Pro Ile Asp His Leu Cys Glu Leu Leu
558 435
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567 Val Arg Lys Ser Gln Phe Arg Leu Pro Phe Lys Ala Thr Thr Pro Val
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573 Leu Leu Tyr Tyr Gly Cys Arg Arg Ser Asp Glu Asp Tyr Leu Tyr Arg
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575 Glu Glu Leu Ala Gln Phe His Arg Asp Gly Ala Leu Thr Gln Leu Asn
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577 Val Ala Phe Ser Arg Glu Gln Ser His Lys Val Tyr Val Gln His Leu
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579 Leu Lys Gln Asp Arg Glu His Leu Trp Lys Leu Ile Glu Gly Gly Ala
581 His Ile Tyr Val Cys Gly Asp Ala Arg Asn Met Ala Arg Asp Val Gln
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583 Asn Thr Phe Tyr Asp Ile Val Ala Glu Leu Gly Ala Met Glu His Ala
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Gln Ala Val Asp Tyr Ile Lys Lys

erromary Summary

eitern

645

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RAW SEQUENCE LISTING
                                                              DATE: 12/22/2004
                     PATENT APPLICATION: US/09/487,841
                                                              TIME: 15:09:45
                                                                           SAMIC
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                     Output Set: N:\CRF4\12222004\1487841.raw
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     649 <211> LENGTH: 18
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     690 <212> TYPE: PRT
     691 <213> ORGANISM: Aspergillus niger
     693 <400> SEQUENCE: 30
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     698 <212> TYPE: PRT
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     701 <400> SEQUENCE: 31
E--> 702
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Cys Pro Met Val Leu Val Phe Gly Cys Arg Gln Ser Lys Ile Asp His 1
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     705 <211> LENGTH: 18
     706 <212> TYPE: PRT
     707 <213> ORGANISM: Homo sapiens
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709 <400> SEQUENCE: 32

Gly Arg Met Thr Leu Val Phe Gly Cys Arg Arg Pro Asp Glu Asp His 1

712 <210> SEQ ID NO: 33

SAM? Er Du

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RAW SEQUENCE LISTING
                                                              DATE: 12/22/2004
                     PATENT APPLICATION: US/09/487,841
                                                              TIME: 15:09:45
                     Input Set : A:\seqlist.txt
                     Output Set: N:\CRF4\12222004\I487841.raw
     713 <211> LENGTH: 18
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     715 <213> ORGANISM: Homo sapiens
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     722 <212> TYPE: PRT
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     725 <400> SEQUENCE: 34
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Gly Arg Met Thr Leu Val Phe Gly Cys Arg His Pro Glu Glu Asp His 1
     728 <210> SEQ ID NO: 35
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     733 <400> SEQUENCE: 35
E--> 734
Gly Asp Met Ile Leu Leu Phe Gly Cys Arg His Pro Asp Met Asp His 1
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     738 <212> TYPE: PRT
     739 <213> ORGANISM: Escherichia coli
     741 <400> SEQUENCE: 36
E--> 742
Gly Lys Asn Trp Leu Phe Phe Gly Asn Pro His Phe Thr Glu Asp Phe 1
                                                                                  5
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     746 <212> TYPE: PRT
     747 <213> ORGANISM: Saccharomyces cerevisiae
     749 <400> SEQUENCE: 37
E--> 750
Gly Glu Val Phe Leu Tyr Leu Gly Ser Arg His Lys Arg Glu Glu Tyr 1
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     752 <210> SEQ ID NO: 38
     753 <211> LENGTH: 18
     754 <212> TYPE: PRT
     755 <213> ORGANISM: Thiocapsa roseopersicina
     757 <400> SEQUENCE: 38
Gly Arg Asn Trp Leu Ile Phe Gly Asn Arg His Phe His Arg Asp Phe 1
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     762 <212> TYPE: PRT
     763 <213> ORGANISM: Pisum sativum
    765 <400> SEQUENCE: 39
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Gly Leu Ala Trp Leu Phe Leu Gly Val Ala Asn Val Asp Ser Leu Leu 1
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    769 <211> LENGTH: 18
    770 <212> TYPE: PRT
    771 <213> ORGANISM: Spinacia oleracea
    773 <400> SEQUENCE: 40
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E--> 774

Gly Leu Ala Trp Leu Phe Leu Gly Val Pro Thr Ser Ser Leu Leu 1

818 <210> SEQ ID NO: 42 819 <211> LENGTH: 698 SAMP 5

Input Set : A:\seqlist.txt

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826	Ala	Ile	Ala	Glu	Glu	Ile	Cys	Glu	Gln	Ala	Val	۷al	His	Gly	Phe	Ser
827				20					25					30		
828	Ala	Asp	Leu	His	Cys	Ile	Ser	Glu	Ser	Asp	Lys	Tyr	Asp	Leu	Lys	Thr
829			35					40					45			
830	Glu	Thr	Ala	Pro	Leu	Val	Val	Val	Val	Ser	Thr	Thr	Gly	Thr	Gly	Asp
831		50					55					60			_	_
832		Pro	Asp	Thr	Ala	_	Lys	Phe	۷al	Lys		Ile	Gln	Asn	Gln	
833						70		•	_	_	75		_	_	~-3	80
834	Leu	Pro	Val	Asp		Phe	Ala	His	Leu	_	Tyr	GLY	Leu	Leu		Leu
835	au à	_ <	_	~- T	85	1		-1	~	90	~ 3	~ 1		- 1 -	95	
836	GTA	Asp	ser			Thr	Tyr	Pne		Asn	GIY	GLY	ьуs		шe	Asp
837		•	.	100		.	a 1	77-	105	TT -	D1	Ш	7	110	a1	T7
838	гÀг	Arg		GIN	GIU	ьeu	GIY		arg	HIS	Pne	туг	_	THY	GIY	HIS
839	77.	7 ~~~	115	0	ר בעד	αi	т	120	T 011	17a]	37 n 3	C1.,	125	Пжж	т1о	77.7
840	Ата	130	Asp	Cys	vai	GIY	135	GIU	Leu	val	vai	140	PIO	пр	TTE	Ата
842	Clar		Trn	Dro	777 2	T.011		Lare	шic	Dho	Ara		Sar	Δra	Glv	Gln
843	_	пец	тгр	FIO	Ата	150	AT 9	цуз	1113	THE	155	DCI	DCI	nrg	OT y	160
844		Glu	Tle	Ser	Glv		T.en	Pro	Val	Δla		Pro	Δla	Ser	Len	
845	GIG	OIG	110	501	165	1114	шец	110	vai	170	001	110	1114	D01	175	3
	Thr	Asp	Leu	Val		Ser	Glu	Leu	Leu		Ile	Glu	Ser	Gln		Glu
847				180	-1-				185					190		
848	Leu	Leu	Arq	Phe	Asp	Asp	Ser	Gly	Arg	Lys	Asp	Ser	Glu	Val	Leu	Lys
849			195		-	-		200	_	_	-		205			
850	Gln	Asn	Ala	Val	Asn	Ser	Asn	Gln	Ser	Asn	Val	Val	Ile	Glu	Asp	Phe
851		210					215					220				
852	Glu	Ser	Ser	Leu	Thr	Arg	Ser	Val	Pro	Pro	Leu	Ser	Gln	Ala	Ser	Leu
853						230					235					240
854	Asn	Ile	Pro	Gly	Leu	Pro	Pro	Glu	Tyr	Leu	Gln	Val	His	Leu	Gln	Glu
855					245					250	_	_		_	255	
856	Ser	Leu	Gly		Glu	Glu	Ser	Gln		Ser	Val	Thr	Ser		Asp	Pro
857	_	_		260			_	_	265			_	_,	270	_	_
858	Val	Phe		Val	Pro	Ile	Ser	-	Ala	Val	GIn	Leu		Thr	Asn	Asp
859		_	275	_:		_	_	280	~ 3	_	_	3	285	_	1	_
	Ala		Lys	Thr	Thr	Leu		Val	Glu	Leu	Asp		ser	Asn	Thr	Asp
861	_,	290		~-7	_	~7	295		m 1	_	1	300	a .	ъ.		Q
		ser	Tyr	Gin	Pro	_	Asp	Ala	Phe	ser		тте	Cys	Pro	Asn	
863		0	a1	77-7	41 -	310	T 0	т	<i>م</i> ا ۳	71 ***	315	C1 n	T 011	C1.,	7 an	320
864 865	Asp	ser	GIU	val		ser	ьeu	ьeu	GIII		ьeu	GIII	ьeu	GIU		пув
865 866	71	C1	u-l-	C1.~	325	T 033	T 011	T ***	т1 -	330	7/1 ~	λαν	Thr	Larc	335	Laze
	Arg	GIU	пты	340	val	ьeu	пец	пув	345	пуs	мта	Toh	TIIT	цуS 350	пур	цγъ
867 868	C117	Δl =	Thr		Dro	Gl n	ніс	Tle		د 1 ۵	Glv	Cvc	Ser		Gln	Phe
869	сту	мта	355	⊥eu	-10	GIII	1112	360	FIU	та	U⊥Y	Cys	365		0111	T 11C
007			222					200					202	•		

Input Set : A:\seqlist.txt

Output Set: N:\CRF4\12222004\I487841.raw

```
870 Ile Phe Thr Trp Cys Leu Glu Ile Arg Ala Ile Pro Lys Lys Ala Phe
            370
                                375
     872 Leu Arg Ala Leu Val Asp Tyr Thr Ser Asp Ser Ala Glu Lys Arg Arg
                            390
                                               395
     874 Leu Gln Glu Leu Cys Ser Lys Gln Gly Ala Ala Asp Tyr Ser Arg Phe
                        405
     876 Val Arg Asp Ala Cys Ala Cys Leu Leu Asp Leu Leu Leu Ala Phe Pro
                    420 ·
                                        425
    878 Ser Cys Gln Pro Pro Leu Ser Leu Leu Glu His Leu Pro Lys Leu
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         435
    880 Gln Pro Arg Pro Tyr Ser Cys Ala Ser Ser Leu Phe His Pro Gly
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                               455
                                                   460
    882 Lys Leu His Phe Val Phe Asn Ile Val Glu Phe Leu Ser Thr Ala Thr
                           470
    884 Thr Glu Val Leu Arg Lys Gly Val Cys Thr Gly Trp Leu Ala Leu Leu
                        485
                                            490
     886 Val Ala Ser Val Leu Gln Pro Asn Ile His Ala Ser His Glu Asp Ser
                                        505
    888 Gly Lys Ala Leu Ala Pro Lys Ile Ser Ile Ser Pro Arg Thr Thr Asn
                515
                                    520
                                                       525
    890 Ser Phe His Leu Pro Asp Asp Pro Ser Ile Pro Ile Ile Met Val Gly
                               535
    892 Pro Gly Thr Gly Ile Ala Pro Phe Ile Gly Phe Leu Gln His Arg Glu
                            550
                                               555
    894 Lys Leu Gln Glu Gln His Pro Asp Gly Asn Phe Gly Ala Met Trp Leu
                       565
                                           570
    896 Phe Phe Gly Cys Arg His Lys Asp Arg Asp Tyr Leu Phe Arg Lys Glu
                    580
                                       585
    898 Leu Arg His Phe Leu Lys His Gly Ile Leu Thr His Leu Lys Val Ser
                595
                                    600
    900 Phe Ser Arg Asp Ala Pro Val Gly Glu Glu Ala Pro Ala Lys Tyr
                                615
    902 Val Gln Asp Asn Ile Gln Leu His Gly Gln Gln Val Ala Arg Ile Leu
                        - 630
     904 Leu Gln Glu Asn Gly His Ile Tyr Val Cys Gly Asp Ala Lys Asn Met
                        645
                                           650
                                                                    675 PVW
    906 Ala Lys Asp Val His Asp Ala Leu Val Gln Ile Ile Ser Lys Glu Val
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                    660
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    952 <210> SEQ ID NO: 44
    953 <211> LENGTH: 698
    954 <212> TYPE: PRT
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    957 <400> SEQUENCE: 44
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962 Ala Asp Leu His Thr Ile Ser Glu Ser Asp Lys Tyr Asp Leu Lys Thr

20

Input Set : A:\seqlist.txt

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966 Pro Pro	Asp Thr	Ala Arg	Lys	Phe	Val	Lys	Glu	Ile	Gln	Asn	Gln	Thr
967 65		. 70					75					80
968 Leu Pro	Val Asp	Phe Phe	Ala	His	Leu	Arg	Tyr	Gly	Leu	Leu	Gly	Leu
969	_	85				90	-	-			95	
970 Gly Asp	Ser Glu	Tyr Thr	Tyr	Phe	Cys	Asn	Gly	Gly	Lys	Ile	Ile	Asp
971	100	_	-		105		-	-	_	110		_
972 Lys Arg	Leu Gln	Glu Leu	Gly	Ala	Arq	His	Phe	Tyr	Asp	Thr	Gly	His
973	115		_	120	_			-	125		_	
974 Ala Asp	Asp Cys	Val Gly	Leu	Glu	Leu	Val	Val	Glu	Pro	Trp	Ile	Ala
975 130		_	135					140		_		
976 Gly Leu	Trp Pro	Ala Leu	Arg	Lys	His	Phe	Arg	Ser	Ser	Arg	Gly	Gln
977 145	_	150	_	_			155					160
978 Glu Glu	Ile Ser	Gly Ala	Leu	Pro	Val	Ala	Ser	Pro	Ala	Ser	Leu	Arg
979		165				170					175	_
980 Thr Asp	Leu Val	Lys Ser	Glu	Leu	Leu	His	Ile	Glu	Ser	Gln	Val	Glu
981	180	_			185					190		
982 Leu Leu	Arg Phe	Asp Asp	Ser	Gly	Arg	Lys	Asp	Ser	Glu	Val	Leu	Lys
983	195			200	_	_	_		205			
984 Gln Asn	Ala Val .	Asn Ser	Asn	Gln	Ser	Asn	Val	Val	Ile	Glu	Asp	Phe
985 210			215					220				
986 Glu Ser	Ser Leu	Thr Arg	Ser	Val	Pro	Pro	Leu	Ser	Gln	Ala	Ser	Leu
987 225		230					235					240
988 Asn Ile	Pro Gly	Leu Pro	Pro	Glu	Tyr	Leu	Gln	Val	His	Leu	Gln	Glu
989		245				250					255	
990 Ser Leu	Gly Gln	Glu Glu	Ser	Gln	Val	Ser	Val	Thr	Ser	Ala	Asp	Pro
991	260				265					270		
992 Val Phe	Gln Val	Pro Ile	Ser	Lys	Ala	Val	Gln	Leu	Thr	Thr	Asn	Asp
993	275			280					285			
994 Ala Ile	Lys Thr	Thr Leu	Leu	Val	Glu	Leu	Asp	Ile	Ser	Asn	Thr	Asp
995 290			295					300				
996 Phe Ser	Tyr Gln	Pro Gly	Asp	Ala	Phe	Ser	Val	Ile	Cys	Pro	Asn	Ser
997 305		310					315					320
998 Asp Ser	Glu Val	Gln Ser	Leu	Leu	Gln	Arg	Leu	Gln	Leu	Glu	Asp	Lys
999		325				330					335	
1000 Arg Gl	u His Cys	Val Leu	ı Leu	. Lys	Ile	Lys	: Ala	ı Asp	Thr	Lys	Lys	Lys
1001	340				345					350		
1002 Gly Al	a Thr Leu	Pro Glr	His	Ile	Pro	Ala	ı Gly	г Сув	Ser	Lei	ı Glr	ı Phe
1003	355			360					365			
1004 Ile Ph	e Thr Trp	Cys Let	ı Glu	Ile	Arg	, Ala	ılle	Pro	Lys	Lys	s Ala	Phe
1005 37	0		375					380)			
1006 Leu Ar	g Ala Leu	Val Asp	Tyr	Thr	Ser	Asp	Ser	Ala	Glu	ı Lys	a Arg	, Arg
1007 385		390					395					400
1008 Leu Gl	n Glu Leu	Cys Ser	Lys	Gln	Gly	Ala	a Alá	Asp	Tyr	Ser	: Arg	J Phe
1009		405				410)			_	415	5
1010 Val Ar	g Asp Ala	Cys Ala	Cys	Leu	Leu	ı Asp	Leu	ı Lev	Let	ı Ala	a Phe	Pro
1011	420				425	<u>, </u>				430)	

Input Set : A:\seqlist.txt

Output Set: N:\CRF4\12222004\I487841.raw

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     1016 Lys Leu His Phe Val Phe Asn Ile Val Glu Phe Leu Ser Thr Ala Thr
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                                                  475
    1018 Thr Glu Val Leu Arg Lys Gly Val Cys Thr Gly Trp Leu Ala Leu Leu
                         485
                                              490
    1020 Val Ala Ser Val Leu Gln Pro Asn Ile His Ala Ser His Glu Asp Ser
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                                          505
    1022 Gly Lys Ala Leu Ala Pro Lys Ile Ser Ile Ser Pro Arg Thr Thr Asn
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    1024 Ser Phe His Leu Pro Asp Asp Pro Ser Ile Pro Ile Ile Met Val Gly
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    1026 Pro Gly Thr Gly Ile Ala Pro Phe Ile Gly Phe Leu Gln His Arg Glu
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    1027 545
                              550
     1028 Lys Leu Gln Glu Gln His Pro Asp Gly Asn Phe Gly Ala Met Trp Leu
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                                              570
     1030 Phe Phe Gly Cys Arg His Lys Asp Arg Asp Tyr Leu Phe Arg Lys Glu
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    1032 Leu Arg His Phe Leu Lys His Gly Ile Leu Thr His Leu Lys Val Ser
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                                      600
    1034 Phe Ser Arg Asp Ala Pro Val Gly Glu Glu Ala Pro Ala Lys Tyr
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    1036 Val Gln Asp Asn Ile Gln Leu His Gly Gln Gln Val Ala Arg Ile Leu
    1037 625
                             630
                                                  635
    1038 Leu Gln Glu Asn Gly His Ile Tyr Val Cys Gly Asp Ala Lys Asn Met
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    1040 Ala Lys Asp Val His Asp Ala Leu Val Gln Ile Ile Ser Lys Glu Val
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                                                              670
E--> 1042
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C80

Gly Val Glu Lys Leu Glu Ala Met Lys Thr Leu Ala Thr Leu Lys Glu

1086 <210> SEQ ID NO: 46

1087 <211> LENGTH: 697

1088 <212> TYPE: PRT

1089 <213> ORGANISM: Homo sapiens

1091 <400> SEQUENCE: 46

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1103 90

1104 Gly Asp Ser Glu Tyr Thr Tyr Phe Cys Asn Gly Gly Lys Ile Ile Asp

Input Set : A:\seqlist.txt

									105					110		
1105	T	. 7	Ŧ	100	a 1	.		77-	105	TT 2	Dh.a	m	7	110	C1	ніс
1106	ьўs	Arg		GIn	GIU	Leu	GLY		Arg	HIS	Pne	IÀT		TIIT	Gry	птъ
1107		_	115			~ 1	.	120	.	77-7	77- J	<u>ما</u>	125	Ш	T1.	77.
1108	Ата		Asp	Cys	vaı	GIY		GIU	Leu	vai	vai		PLO	пр	тте	Ата
1109	7	130	_	_	~ 7		135	.		D1	3	140	a	7	a 3	d1
1110		Leu	Trp	Pro	Ala		Arg	ьуs	His	Pne		Ser	ser	Arg	GIY	
1111						150	_	_			155	_		~	_	160
1112	Glu	GIu	He	Ser		Ala	Leu	Pro	Val		Ser	Pro	Ата	ser		Arg
1113					165				_	170			_		175	~ 3
1114	Thr	Asp	Leu			Ser	Glu	Leu		His	Ile	Glu	Ser		Val	Glu
1115				180					185					190	_	_
1116	Leu	Leu		Phe	Asp	Asp	Ser		Arg	Lys	Asp	Ser		Val	Leu	ьуs
1117			195					200				_	205	_		
1118	Gln		Ala	Val	Asn	Ser		Gln	Ser	Asn	Val		Ile	Glu	Asp	Phe
1119		210					215					220	_			
1120	Glu	Ser	Ser	Leu	Thr	_	Ser	Val	Pro	Pro		Ser	Gln	Ala	Ser	
1121						230					235				_	240
1122	Asn	Ile	Pro	Gly	Leu	Pro	Pro	Glu	Tyr		Gln	Val	His	Leu		Glu
1123					245					250					255	
1124	Ser	Leu	Gly	Gln	Glu	Glu	Ser	Gln		Ser	Val	Thr	Ser		Asp	Pro
1125				260					265		_			270		
1126	Val	Phe	Gln	Val	Pro	Ile	Ser	_	Ala	Val	Gln	Leu		Thr	Asn	Asp
1127			275					280					285			
1128	Ala	Ile	Lys	Thr	Thr	Leu		Val	Glu	Leu	Asp	Ile	Ser	Asn	Thr	Asp
1129		290					295					300				
1130	Phe	Ser	Tyr	Gln	Pro	Gly	Asp	Ala	Phe	Ser		Ile	Cys	Pro	Asn	
1131						310					315					320
1132	Asp	Ser	Glu	Val	Gln	Ser	Leu	Leu	Gln		Leu	Gln	Leu	Glu		Lys
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1134	Arg	Glu	His	_	Val	Leu	Leu	Lys		Lys	Ala	Asp	Thr		Lys	Lys
1135				340					345					350	_	_
1136	Gly	Ala	Thr	Leu	Pro	Gln	His		Pro	Ala	Gly	Cys		Leu	Gln	Phe
1137			355					360		_	_		365			
1138	Ile	Phe	Thr	Trp	Cys	Leu		Ile	Arg	Ala	Ile		Lys	Lys	Ala	Phe
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1140	Leu	Arg	Ala	Leu	Val		Tyr	Thr	Ser	Asp		Ala	Glu	Lys	Arg	
1141						390					395					400
1142	Leu	Gln	Glu	Leu	Cys	Ser	Lys	Gln	Gly	Ala	Ala	Asp	Tyr	Ser		Phe
1143					405					410				_	415	
1144	Val	Arg	Asp	Ala	Cys	Ala	Cys	Leu		Asp	Leu	Leu	Leu		Phe	Pro
1145				420					425					4 30		
1146	Ser	Cys	Gln	Pro	Pro	Leu	Ser		Leu	Leu	Glu	His	Leu	Pro	Lys	Leu
1147			435					440					445	•		
1148	Gln	Pro	Arg	Pro	Tyr	Ser	Cys	Ala	Ser	Ser	Ser		Phe	His	Pro	Gly
1149		450					455					460				_
1150		Leu	His	Phe	Val	Phe	Asn	Ile	Val	Glu		Leu	Ser	Thr	Ala	
1151						470					475					480
1152	Thr	Glu	Val	Leu	Arg	Lys	Gly	Val	Cys	Thr	Gly	Trp	Leu	Ala		Leu
1153					485					490					495	
	,															

Input Set : A:\seqlist.txt
Output Set: N:\CRF4\12222004\1487841.raw

1154 Val Ala Ser Val Leu Gln Pro Asn Ile His Ala Ser His Glu Asp Ser 500 505 1155 1156 Gly Lys Ala Leu Ala Pro Lys Ile Ser Ile Ser Pro Arg Thr Thr Asn 520 525 515 1158 Ser Phe His Leu Pro Asp Asp Pro Ser Ile Pro Ile Ile Met Val Gly 535 1160 Pro Gly Thr Gly Ile Ala Pro Phe Ile Gly Phe Leu Gln His Arg Glu 555 550 1162 Lys Leu Gln Glu Gln His Pro Asp Gly Asn Phe Gly Ala Met Trp Phe 565 570 1164 Phe Gly Cys Arg His Lys Asp Arg Asp Tyr Leu Phe Arg Lys Glu Leu 580 585 1166 Arg His Phe Leu Lys His Gly Ile Leu Thr His Leu Lys Val Ser Phe 595 600 1168 Ser Arg Asp Ala Pro Val Gly Glu Glu Glu Ala Pro Ala Lys Tyr Val 615 620 1170 Gln Asp Asn Ile Gln Leu His Gly Gln Gln Val Ala Arg Ile Leu Leu 630 635 1172 Gln Glu Asn Gly His Ile Tyr Val Cys Gly Asp Ala Lys Asn Met Ala 645 650 1174 Lys Asp Val His Asp Ala Leu Val Gln Ile Ile Ser Lys Glu Val Gly 1175 660 665 E--> 1176 Val Glu Lys Leu Glu Ala Met Lys Thr Leu Ala Thr Leu Lys Glu Glu

Sprend

680

RAW SEQUENCE LISTING ERROR SUMMARY

DATE: 12/22/2004

PATENT APPLICATION: US/09/487,841

TIME: 15:09:46

Input/Set : A:\seqlist.txt

Output Set: N:\CRF4\12222004\I487841.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

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Seq#:22; Line(s) 495
Seq#:23; Line(s) 584
Seq#:25; Line(s) 654
Seq#:26; Line(s) 662
Seq#:27; Line(s) 670
Seq#:28; Line(s) 678
Seq#:29; Line(s) 686
Seq#:30; Line(s) 694
Seq#:31; Line(s) 702
Seq#:32; Line(s) 710
Seq#:33; Line(s) 718
Seq#:34; Line(s) 726
Seq#:35; Line(s) 734
Seq#:36; Line(s) 742
Seq#:37; Line(s) 750
Seq#:38; Line(s) 758
Seq#:39; Line(s) 766
Seq#:40; Line(s) 774
Seq#:42; Line(s) 908
Seq#:44; Line(s) 1042
Seq#:46; Line(s) 1176
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/487,841

DATE: 12/22/2004 TIME: 15:09:46

Input Set : A:\seqlist.txt

Output Set: N:\CRF4\12222004\I487841.raw

L:405 M:252 E: No. of Seq. differs, <211> LENGTH:Input:698 Found:672 SEQ:21 L:495 M:252 E: No. of Seq. differs, <211> LENGTH:Input:682 Found:656 SEQ:22 L:584 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:23 L:584 M:252 E: No. of Seq. differs, <211> LENGTH:Input:677 Found:656 SEQ:23 L:654 M:333 E: Wrong sequence grouping, Amino acids not in groups! L:662 M:333 E: Wrong sequence grouping, Amino acids not in groups! L:670 M:333 E: Wrong sequence grouping, Amino acids not in groups! L:678 M:333 E: Wrong sequence grouping, Amino acids not in groups! L:686 M:333 E: Wrong sequence grouping, Amino acids not in groups! L:694 M:333 E: Wrong sequence grouping, Amino acids not in groups! L:702 M:333 E: Wrong sequence grouping, Amino acids not in groups! L:710 M:333 E: Wrong sequence grouping, Amino acids not in groups! L:718 M:333 E: Wrong sequence grouping, Amino acids not in groups! L:726 M:333 E: Wrong sequence grouping, Amino acids not in groups! L:734 M:333 E: Wrong sequence grouping, Amino acids not in groups! L:742 M:333 E: Wrong sequence grouping, Amino acids not in groups! L:750 M:333 E: Wrong sequence grouping, Amino acids not in groups! L:758 M:333 E: Wrong sequence grouping, Amino acids not in groups! L:766 M:333 E: Wrong sequence grouping, Amino acids not in groups! L:774 M:333 E: Wrong sequence grouping, Amino acids not in groups! L:908 M:252 E: No. of Seq. differs, <211> LENGTH:Input:698 Found:672 SEQ:42 L:1042 M:252 E: No. of Seq. differs, <211> LENGTH:Input:698 Found:672 SEQ:44 L:1176 M:252 E: No. of Seq. differs, <211> LENGTH:Input:697 Found:672 SEQ:46